

SEQUENCE LISTING

<110> HIRANO, Seiko
YASUEDA, Hisashi

<120> Novel lysine decarboxylase gene and method for
producing L-lysine

<130> US-109

<150> JP 2003-47185

<151> 2003-02-25

<160> 26

<170> PatentIn Ver. 2.0

<210> 1

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 1

gcgagctcag cgcgagtgac tggatatcgg a

31

<210> 2

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 2

gcggtaccac tgtataaata gcaaaggcaa c

31

<210> 3

<211> 2964

<212> DNA

<213> Methylophilus methylotrophus

<220>

<221> CDS

<222> (684).. (2930)

<400> 3

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tatggcacct cttcttacgg ttacgatatc cgttgtgctg acgaattccg cgtatttacc 180
aatatcaaca gcaccatagt tgaccccaag caatttgacc cgcagtcgtt tgtcgaggtc 240
tccggcaaag gctattgctg gattccccct aactcatttg cactggcgcg cacggtagag 300
tatttccgta ttctcgcgc tgtactgact gtatgcctcg gcaagtcgac ttatgcgcgt 360
tgoggcatta tcgtcaacgt caccoccttt gaaccagagt gggaaggcta tgtcacacta 420
gagttcagca acaccacacc gctacccgcc aaaatttatg ctggcgaagg ctgtgcgcaa 480
gtgctgttct ttgagtctga tgaatctgt gaaacgagct acaagaccg tgggtgtaaa 540
taccagggtc aaattggcgt gaccctgcc aaaaataaac ggcaacattg aacaataacc 600
tgacattcac caagggcacg gtgcaaagca aatgctttct ctgtgccctt gtgtcttgat 660
tttagcggta aaggatttat tgc atg aaa ttt aga ttc cct atc gtc att att 713

Met Lys Phe Arg Phe Pro Ile Val Ile Ile

1 5 10

gac gag gac ttc cgc tcc gag aac tct tcc ggc ctg ggc atc cgt gtg 761
Asp Glu Asp Phe Arg Ser Glu Asn Ser Ser Gly Leu Gly Ile Arg Val

15 20 25

ctg gcg aaa gcc atc gaa gat gag ggc ctg gaa gtg ctt ggc gtc acc 809
Leu Ala Lys Ala Ile Glu Asp Glu Gly Leu Glu Val Leu Gly Val Thr

30 35 40

agc tat ggc gac ctg acc tct ttc gcc cag cag caa agc cgt gca tca 857
Ser Tyr Gly Asp Leu Thr Ser Phe Ala Gln Gln Gln Ser Arg Ala Ser

45 50 55

gcc ttt atc ctg tcg att gat gat gag gaa atc gtt gag gag aaa ccg	905
Ala Phe Ile Leu Ser Ile Asp Asp Glu Glu Ile Val Glu Glu Lys Pro	
60 65 70	
gaa gcc att gag caa ctg cgt aac ttt gtg cag gaa atc cgt tac cgc	953
Glu Ala Ile Glu Gln Leu Arg Asn Phe Val Gln Glu Ile Arg Tyr Arg	
75 80 85 90	
aac gag gaa atc ccc att ttc ctg cat ggc gaa acc cgt acc agc cgt	1001
Asn Glu Glu Ile Pro Ile Phe Leu His Gly Glu Thr Arg Thr Ser Arg	
95 100 105	
cac atc cct aac gat gtg ttg cgc gag ttg cac ggc ttt atc cat atg	1049
His Ile Pro Asn Asp Val Leu Arg Glu Leu His Gly Phe Ile His Met	
110 115 120	
aat gaa gac acg cct gag ttt gtg gcg cgc ctg att atc cgc gaa gcc	1097
Asn Glu Asp Thr Pro Glu Phe Val Ala Arg Leu Ile Ile Arg Glu Ala	
125 130 135	
aaa gcc tac ctg gac agc ttg cca ccg ccc ttc ttc aag gca ctc act	1145
Lys Ala Tyr Leu Asp Ser Leu Pro Pro Pro Phe Phe Lys Ala Leu Thr	
140 145 150	
cat tac gcg gct gat ggc tct tat tca tgg cac tgt cct ggt cac tcg	1193
His Tyr Ala Ala Asp Gly Ser Tyr Ser Trp His Cys Pro Gly His Ser	
155 160 165 170	
ggc gta gcc ttt ctg aaa tcc cca gtc ggg cag atg ttc cac cag	1241
Gly Gly Val Ala Phe Leu Lys Ser Pro Val Gly Gln Met Phe His Gln	
175 180 185	
ttt ttt ggc gag aac atg ctg cgt gca gac gtg tgt aat gcg gta gat	1289
Phe Phe Gly Glu Asn Met Leu Arg Ala Asp Val Cys Asn Ala Val Asp	
190 195 200	
gaa tta ggc caa tta ctg gat cac acc ggc ccg gtg gcc gct tct gag	1337
Glu Leu Gly Gln Leu Leu Asp His Thr Gly Pro Val Ala Ala Ser Glu	
205 210 215	
cgc aac gct gcg cgc atc tac aac tgc gac cat ttg tac ttt gtc act	1385
Arg Asn Ala Ala Arg Ile Tyr Asn Cys Asp His Leu Tyr Phe Val Thr	
220 225 230	
aac ggc acc tca aca tcg aac aag att gtc tgg aac tca acc gtg gcg	1433
Asn Gly Thr Ser Thr Ser Asn Lys Ile Val Trp Asn Ser Thr Val Ala	
235 240 245 250	

cgc ggt gat att gta gtg gtt gat cgt aac tgc cat aaa tcc gta ttg	1481
Pro Gly Asp Ile Val Val Val Asp Arg Asn Cys His Lys Ser Val Leu	
255 260 265	
cac tcc atc att atg acg ggt gcc gtg ccc gtg ttc ctg atg cca acg	1529
His Ser Ile Ile Met Thr Gly Ala Val Pro Val Phe Leu Met Pro Thr	
270 275 280	
cgc aac cat ttc ggc att atc ggg cct atc cca aaa agt gaa ttc gcc	1577
Arg Asn His Phe Gly Ile Ile Gly Pro Ile Pro Lys Ser Glu Phe Ala	
285 290 295	
tgg gaa aac atc cag aaa aag atc gca cgc aac ccg ttt gcc acc gac	1625
Trp Glu Asn Ile Gln Lys Lys Ile Ala Arg Asn Pro Phe Ala Thr Asp	
300 305 310	
aaa aat gcc aag cca cgc gtg ctg acc att aca cag tcc acc tat gat	1673
Lys Asn Ala Lys Pro Arg Val Leu Thr Ile Thr Gln Ser Thr Tyr Asp	
315 320 325 330	
ggc gtg ttg tat aac gtg gaa gaa atc aag gaa atg ctg gat ggc aaa	1721
Gly Val Leu Tyr Asn Val Glu Glu Ile Lys Glu Met Leu Asp Gly Lys	
335 340 345	
att gac acc ctg cac ttt gac gaa gcc tgg ttg cca cat gcg acc ttc	1769
Ile Asp Thr Leu His Phe Asp Glu Ala Trp Leu Pro His Ala Thr Phe	
350 355 360	
cat gac ttt tat ggt gac tac cat gcg att ggc gct gac cgc cca cgc	1817
His Asp Phe Tyr Gly Asp Tyr His Ala Ile Gly Ala Asp Arg Pro Arg	
365 370 375	
tgt aaa gaa tcc atg gtg ttc tcc acc cag tcc acg cac aaa cta ttg	1865
Cys Lys Glu Ser Met Val Phe Ser Thr Gln Ser Thr His Lys Leu Leu	
380 385 390	
gca ggc cta agc cag gcc tcg cag att ctg gta cag gat gcc gac cag	1913
Ala Gly Leu Ser Gln Ala Ser Gln Ile Leu Val Gln Asp Ala Asp Gln	
395 400 405 410	
aac cgc ctg gac cgt gac gtg ttc aac gaa gcc tat ttg atg cac acc	1961
Asn Arg Leu Asp Arg Asp Val Phe Asn Glu Ala Tyr Leu Met His Thr	
415 420 425	
tcc acc agc ccg caa tat tca att att gcc agc tgc gac gtc gct gct	2009
Ser Thr Ser Pro Gln Tyr Ser Ile Ile Ala Ser Cys Asp Val Ala Ala	
430 435 440	

gcc atg atg gaa gcc cct ggt ggc acc gcc ctg gta gaa gaa tcc ctc	2057
Ala Met Met Glu Ala Pro Gly Gly Thr Ala Leu Val Glu Glu Ser Leu	
445 450 455	
aaa gaa gcg ttg gac ttc cgc cgc gcc atg cgc aag gtc gac gaa gaa	2105
Lys Glu Ala Leu Asp Phe Arg Arg Ala Met Arg Lys Val Asp Glu Glu	
460 465 470	
tgg ggc aca gac tgg tgg ttt aaa gtc tgg ggt cca act gac ctg tcc	2153
Trp Gly Thr Asp Trp Trp Phe Lys Val Trp Gly Pro Thr Asp Leu Ser	
475 480 485 490	
gaa gac ggc ctg gaa gaa cgt gac gcg tgg atg ctc aaa gcc aat gaa	2201
Glu Asp Gly Leu Glu Glu Arg Asp Ala Trp Met Leu Lys Ala Asn Glu	
495 500 505	
cgc tgg cat ggc ttc ggc aac ctg gcc gaa ggc ttt aac atg ctg gat	2249
Arg Trp His Gly Phe Gly Asn Leu Ala Glu Gly Phe Asn Met Leu Asp	
510 515 520	
ccg atc aaa gcc acc atc atc acc cca gga cta gac gta gaa ggc gac	2297
Pro Ile Lys Ala Thr Ile Ile Thr Pro Gly Leu Asp Val Glu Gly Asp	
525 530 535	
ttt tcc gat gaa ttc ggc atc ccc gct gcc att gtc acc aag tac ctg	2345
Phe Ser Asp Glu Phe Gly Ile Pro Ala Ala Ile Val Thr Lys Tyr Leu	
540 545 550	
gct gaa cac ggt gtg atc gtt gaa aaa acc ggt tta tac tca ttc ttt	2393
Ala Glu His Gly Val Ile Val Glu Lys Thr Gly Leu Tyr Ser Phe Phe	
555 560 565 570	
atc atg ttc acc atc ggc att acc aaa ggc cgc tgg aac acg atg gtg	2441
Ile Met Phe Thr Ile Gly Ile Thr Lys Gly Arg Trp Asn Thr Met Val	
575 580 585	
gcc gcg tta caa caa ttt aaa gac gac tac gac aag aat cag ccg ctg	2489
Ala Ala Leu Gln Gln Phe Lys Asp Asp Tyr Asp Lys Asn Gln Pro Leu	
590 595 600	
tgg aaa gtg ctg cct gag ttt gta cag aaa cat cca cgc tat gaa cgc	2537
Trp Lys Val Leu Pro Glu Phe Val Gln Lys His Pro Arg Tyr Glu Arg	
605 610 615	
gta ggc ctg aaa gat cta tgc acg cag att cat gaa gtt tac aaa gct	2585
Val Gly Leu Lys Asp Leu Cys Thr Gln Ile His Glu Val Tyr Lys Ala	
620 625 630	

aac gac gta gca cgc ctg acc aca gaa atg tac ctg tot gac atg gtg 2633
 Asn Asp Val Ala Arg Leu Thr Thr Glu Met Tyr Leu Ser Asp Met Val
 635 640 645 650
 cca gcc atg aaa ccg acc gat gct ttc tca aaa atg gcg cat cgc aaa 2681
 Pro Ala Met Lys Pro Thr Asp Ala Phe Ser Lys Met Ala His Arg Lys
 655 660 665
 att gaa cgc gta gcc att gat gac ctc gaa ggc cgc gtc act gca gtg 2729
 Ile Glu Arg Val Ala Ile Asp Asp Leu Glu Gly Arg Val Thr Ala Val
 670 675 680
 ctg tta acg ccc tat ccg cca ggc atc ccg ttg ctg atc cct ggc gaa 2777
 Leu Leu Thr Pro Tyr Pro Pro Gly Ile Pro Leu Leu Ile Pro Gly Glu
 685 690 695
 cgc ttt aac aaa gtc att gtg aac tac ctc aag ttt gcg cgc gag ttt 2825
 Arg Phe Asn Lys Val Ile Val Asn Tyr Leu Lys Phe Ala Arg Glu Phe
 700 705 710
 aat gag aaa ttc cca ggc ttt gag acg gat aac cat gga tta gtg aag 2873
 Asn Glu Lys Phe Pro Gly Phe Glu Thr Asp Asn His Gly Leu Val Lys
 715 720 725 730
 caa ata gtc gat ggt aaa gcc gtg tat tat gtg gat tgc gtg aag caa 2921
 Gln Ile Val Asp Gly Lys Ala Val Tyr Tyr Val Asp Cys Val Lys Gln
 735 740 745
 gaa gat taa atttttagtt tcactcagca gtttttctac tgag 2964
 Glu Asp

<210> 4

<211> 748

<212> PRT

<213> Methylophilus methylotrophus

<400> 4

Met Lys Phe Arg Phe Pro Ile Val Ile Ile Asp Glu Asp Phe Arg Ser
 1 5 10 15
 Glu Asn Ser Ser Gly Leu Gly Ile Arg Val Leu Ala Lys Ala Ile Glu
 20 25 30
 Asp Glu Gly Leu Glu Val Leu Gly Val Thr Ser Tyr Gly Asp Leu Thr
 35 40 45
 Ser Phe Ala Gln Gln Gln Ser Arg Ala Ser Ala Phe Ile Leu Ser Ile

50	55	60	
Asp Asp Glu Glu Ile Val	Glu Glu Lys Pro Glu Ala Ile	Glu Gln Leu	
65	70	75	80
Arg Asn Phe Val Gln Glu Ile	Arg Tyr Arg Asn Glu Glu Ile	Pro Ile	
	85	90	95
Phe Leu His Gly Glu Thr Arg Thr	Ser Arg His Ile Pro Asn Asp Val		
	100	105	110
Leu Arg Glu Leu His Gly Phe Ile His	Met Asn Glu Asp Thr Pro Glu		
	115	120	125
Phe Val Ala Arg Leu Ile Ile Arg Glu Ala Lys Ala Tyr	Leu Asp Ser		
	130	135	140
Leu Pro Pro Pro Phe Phe Lys Ala Leu Thr His Tyr Ala Ala Asp Gly			
	145	150	155
Ser Tyr Ser Trp His Cys Pro Gly His Ser Gly Gly Val Ala Phe Leu			
	165	170	175
Lys Ser Pro Val Gly Gln Met Phe His Gln Phe Phe Gly Glu Asn Met			
	180	185	190
Leu Arg Ala Asp Val Cys Asn Ala Val Asp Glu Leu Gly Gln Leu Leu			
	195	200	205
Asp His Thr Gly Pro Val Ala Ala Ser Glu Arg Asn Ala Ala Arg Ile			
	210	215	220
Tyr Asn Cys Asp His Leu Tyr Phe Val Thr Asn Gly Thr Ser Thr Ser			
	225	230	235
Asn Lys Ile Val Trp Asn Ser Thr Val Ala Pro Gly Asp Ile Val Val			
	245	250	255
Val Asp Arg Asn Cys His Lys Ser Val Leu His Ser Ile Ile Met Thr			
	260	265	270
Gly Ala Val Pro Val Phe Leu Met Pro Thr Arg Asn His Phe Gly Ile			
	275	280	285
Ile Gly Pro Ile Pro Lys Ser Glu Phe Ala Trp Glu Asn Ile Gln Lys			
	290	295	300
Lys Ile Ala Arg Asn Pro Phe Ala Thr Asp Lys Asn Ala Lys Pro Arg			
	305	310	315
Val Leu Thr Ile Thr Gln Ser Thr Tyr Asp Gly Val Leu Tyr Asn Val			
	325	330	335
Glu Glu Ile Lys Glu Met Leu Asp Gly Lys Ile Asp Thr Leu His Phe			

340	345	350
Asp Glu Ala Trp Leu Pro His	Ala Thr Phe His Asp Phe Tyr Gly Asp	
355	360	365
Tyr His Ala Ile Gly Ala Asp Arg Pro Arg Cys Lys Glu Ser Met Val		
370	375	380
Phe Ser Thr Gln Ser Thr His Lys Leu Leu Ala Gly Leu Ser Gln Ala		
385	390	395
Ser Gln Ile Leu Val Gln Asp Ala Asp Gln Asn Arg Leu Asp Arg Asp		400
405	410	415
Val Phe Asn Glu Ala Tyr Leu Met His Thr Ser Thr Ser Pro Gln Tyr		
420	425	430
Ser Ile Ile Ala Ser Cys Asp Val Ala Ala Ala Met Met Glu Ala Pro		
435	440	445
Gly Gly Thr Ala Leu Val Glu Glu Ser Leu Lys Glu Ala Leu Asp Phe		
450	455	460
Arg Arg Ala Met Arg Lys Val Asp Glu Glu Trp Gly Thr Asp Trp Trp		
465	470	475
Phe Lys Val Trp Gly Pro Thr Asp Leu Ser Glu Asp Gly Leu Glu Glu		
485	490	495
Arg Asp Ala Trp Met Leu Lys Ala Asn Glu Arg Trp His Gly Phe Gly		
500	505	510
Asn Leu Ala Glu Gly Phe Asn Met Leu Asp Pro Ile Lys Ala Thr Ile		
515	520	525
Ile Thr Pro Gly Leu Asp Val Glu Gly Asp Phe Ser Asp Glu Phe Gly		
530	535	540
Ile Pro Ala Ala Ile Val Thr Lys Tyr Leu Ala Glu His Gly Val Ile		
545	550	555
Val Glu Lys Thr Gly Leu Tyr Ser Phe Phe Ile Met Phe Thr Ile Gly		
565	570	575
Ile Thr Lys Gly Arg Trp Asn Thr Met Val Ala Ala Leu Gln Gln Phe		
580	585	590
Lys Asp Asp Tyr Asp Lys Asn Gln Pro Leu Trp Lys Val Leu Pro Glu		
595	600	605
Phe Val Gln Lys His Pro Arg Tyr Glu Arg Val Gly Leu Lys Asp Leu		
610	615	620
Cys Thr Gln Ile His Glu Val Tyr Lys Ala Asn Asp Val Ala Arg Leu		

625		630		635		640									
Thr	Thr	Glu	Met	Tyr	Leu	Ser	Asp	Met	Val	Pro	Ala	Met	Lys	Pro	Thr
		645							650				655		
Asp	Ala	Phe	Ser	Lys	Met	Ala	His	Arg	Lys	Ile	Glu	Arg	Val	Ala	Ile
		660							665				670		
Asp	Asp	Leu	Glu	Gly	Arg	Val	Thr	Ala	Val	Leu	Leu	Thr	Pro	Tyr	Pro
		675							680				685		
Pro	Gly	Ile	Pro	Leu	Leu	Ile	Pro	Gly	Glu	Arg	Phe	Asn	Lys	Val	Ile
		690							695				700		
Val	Asn	Tyr	Leu	Lys	Phe	Ala	Arg	Glu	Phe	Asn	Glu	Lys	Phe	Pro	Gly
705				710						715				720	
Phe	Glu	Thr	Asp	Asn	His	Gly	Leu	Val	Lys	Gln	Ile	Val	Asp	Gly	Lys
				725						730				735	
Ala	Val	Tyr	Tyr	Val	Asp	Cys	Val	Lys	Gln	Glu	Asp				
				740						745					

<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 5

aaggctgtgc gcaagtgctg ttctttgagt

30

<210> 6

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 6

ccagcctaca caatcgctca agacgtgtaa tgcacgcatg gtagtcacca taaaagtcac 60
ggaa 64

<210> 7

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 7

ggctaattcc catgtcagcc gttaagtgtt ccatgaacta cctcaagttt gcgcgcgagt 60
ttaa 64

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 8

ggttggtatc agtgtagaca cggttgcaag 30

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 9

gcattacacg tcttgagcga ttgtgtaggc 30

<210> 10

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 10

ggaacactta acggctgaca tgggaattag cc

32

<210> 11

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 11

aacctgacat tcaccaaggg cacggtgcaa

30

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 12

tttgcgcaaa agcatcgatt atccttcccc

30

<210> 13

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 13

gccctgcagg agcgcgagtg actggatc gga

33

<210> 14

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 14

gccctgcagg ctgtataaat agcaaaggca ac

32

<210> 15

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 15

gcctgcagta aggaaggatt ttccaggagg aacac

35

<210> 16

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 16

gcctgcagaa gctttgctca ccgcataatc cgtcgcaa

38

<210> 17

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 17

aggaattcc ccgttctgga taatgttttt tgcgccgac

39

<210> 18

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 18

cggaatgcatc tagagttaac ctgcagggtg aaattgttat ccgctcacia ttccacac 58

<210> 19

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 19

catttcctgc aggcaaagga gatgagcgta atggtgatca tggaaatctt cattacaggt 60
ctgc 64

<210> 20

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 20

gggcgagcta gaagagctcc aaaacccgcg aaaactaacc catcaacatc 50

<210> 21

<211> 711

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1).. (711)

<400> 21

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1			5						10				15			
ctt	tta	ctg	tcc	atc	gga	ccg	cag	aat	gta	ctg	gtg	att	aaa	caa	gga	96
Leu	Leu	Leu	Ser	Ile	Gly	Pro	Gln	Asn	Val	Leu	Val	Ile	Lys	Gln	Gly	
			20						25				30			
att	aag	cgc	gaa	gga	ctc	att	gcg	ggt	ctt	ctc	gtg	tgt	tta	att	tct	144
Ile	Lys	Arg	Glu	Gly	Leu	Ile	Ala	Val	Leu	Leu	Val	Cys	Leu	Ile	Ser	
			35						40				45			
gac	gtc	ttt	ttg	ttc	atc	gcc	ggc	acc	ttg	ggc	ggt	gat	ctt	ttg	tcc	192
Asp	Val	Phe	Leu	Phe	Ile	Ala	Gly	Thr	Leu	Gly	Val	Asp	Leu	Leu	Ser	

50	55	60	
aat gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct	240		
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala			
65	70	75	80
tac ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac	288		
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn			
85	90	95	
aag gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc	336		
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro			
100	105	110	
gat gac acg cct ttg ggc ggt tcg gcg gtg gcc act gac acg cgc aac	384		
Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn			
115	120	125	
cgg gtg cgg gtg gag gtg agc gtc gat aag cag cgg gtt tgg gta aag	432		
Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys			
130	135	140	
ccc atg ttg atg gca atc gtg ctg acc tgg ttg aac ccg aat gcg tat	480		
Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr			
145	150	155	160
ttg gac gcg ttt gtg ttt atc ggc ggc gtc ggc gcg caa tac ggc gac	528		
Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp			
165	170	175	
acc gga cgg tgg att ttc gcc gct ggc gcg ttc gcg gca agc ctg atc	576		
Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile			
180	185	190	
tgg ttc ccg ctg gtg ggt ttc ggc gca gca gca ttg tca cgc ccg ctg	624		
Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu			
195	200	205	
tcc agc ccc aag gtg tgg cgc tgg atc aac gtc gtc gtg gca gtt gtg	672		
Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val			
210	215	220	
atg acc gca ttg gcc atc aaa ctg atg ttg atg ggt tag	711		
Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly			
225	230	235	

<210> 22

<211> 236

<212> PRT

<213> Brevibacterium lactofermentum

<400> 22

Met	Val	Ile	Met	Glu	Ile	Phe	Ile	Thr	Gly	Leu	Leu	Leu	Gly	Ala	Ser
1			5					10					15		
Leu	Leu	Leu	Ser	Ile	Gly	Pro	Gln	Asn	Val	Leu	Val	Ile	Lys	Gln	Gly
			20				25						30		
Ile	Lys	Arg	Glu	Gly	Leu	Ile	Ala	Val	Leu	Leu	Val	Cys	Leu	Ile	Ser
	35					40					45				
Asp	Val	Phe	Leu	Phe	Ile	Ala	Gly	Thr	Leu	Gly	Val	Asp	Leu	Leu	Ser
	50					55					60				
Asn	Ala	Ala	Pro	Ile	Val	Leu	Asp	Ile	Met	Arg	Trp	Gly	Gly	Ile	Ala
65					70					75				80	
Tyr	Leu	Leu	Trp	Phe	Ala	Val	Met	Ala	Ala	Lys	Asp	Ala	Met	Thr	Asn
			85						90					95	
Lys	Val	Glu	Ala	Pro	Gln	Ile	Ile	Glu	Glu	Thr	Glu	Pro	Thr	Val	Pro
			100						105					110	
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		115					120							125	
Arg	Val	Arg	Val	Glu	Val	Ser	Val	Asp	Lys	Gln	Arg	Val	Trp	Val	Lys
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Pro	Met	Leu	Met	Ala	Ile	Val	Leu	Thr	Trp	Leu	Asn	Pro	Asn	Ala	Tyr
145				150						155				160	
Leu	Asp	Ala	Phe	Val	Phe	Ile	Gly	Gly	Val	Gly	Ala	Gln	Tyr	Gly	Asp
			165						170					175	
Thr	Gly	Arg	Trp	Ile	Phe	Ala	Ala	Gly	Ala	Phe	Ala	Ala	Ser	Leu	Ile
		180						185						190	
Trp	Phe	Pro	Leu	Val	Gly	Phe	Gly	Ala	Ala	Ala	Leu	Ser	Arg	Pro	Leu
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Ser	Ser	Pro	Lys	Val	Trp	Arg	Trp	Ile	Asn	Val	Val	Val	Ala	Val	Val
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 Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
 20 25 30
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 Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
 35 40 45
 gac gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc 192
 Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
 50 55 60
 aat gcc gcg cgc atc gtg ctc gat att atg cgc tgg ggt ggc atc gct 240
 Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
 65 70 75 80
 tac ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac 288
 Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
 85 90 95
 aag gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc 336
 Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
 100 105 110
 gat gac acg cct ttg ggc gtg ttc ggc ggt ggc cac tga cacgcgcaac 385
 Asp Asp Thr Pro Leu Gly Val Phe Gly Gly Gly His
 115 120 125
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			20					25					30		
Ile	Lys	Arg	Glu	Gly	Leu	Ile	Ala	Val	Leu	Leu	Val	Cys	Leu	Ile	Ser
		35					40					45			
Asp	Val	Phe	Leu	Phe	Ile	Ala	Gly	Thr	Leu	Gly	Val	Asp	Leu	Leu	Ser
	50					55				60					
Asn	Ala	Ala	Pro	Ile	Val	Leu	Asp	Ile	Met	Arg	Trp	Gly	Gly	Ile	Ala
65				70					75					80	
Tyr	Leu	Leu	Trp	Phe	Ala	Val	Met	Ala	Ala	Lys	Asp	Ala	Met	Thr	Asn
			85					90				95			
Lys	Val	Glu	Ala	Pro	Gln	Ile	Ile	Glu	Glu	Thr	Glu	Pro	Thr	Val	Pro
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Asp	Asp	Thr	Pro	Leu	Gly	Val	Phe	Gly	Gly	Gly	His				
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